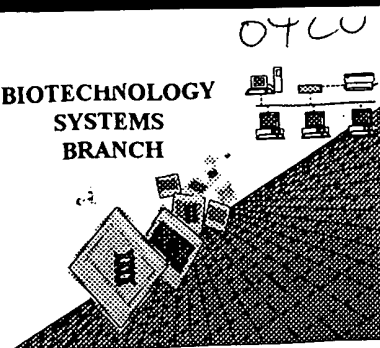


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/884,260
Source: O/E
Date Processed by STIC: 7/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,260

DATE: 07/06/2001

TIME: 11:38:51

Input Set : A:\W054316.txt

Output Set: N:\CRF3\07062001\I884260.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Alan Brash
5 Nathalie Tijet
8 <120> TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
9 LYASE AND USES THEREOF
12 <130> FILE REFERENCE: 06027.0002
C-> 14 <140> CURRENT APPLICATION NUMBER: US/09/884,260
E--> 14 <141> CURRENT FILING DATE: 2001-06-19
E--> 14 <160> NUMBER OF SEQ ID NOS: (57) 56 (see next page)
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

09/884, 260

2

<210> 56
<211> 1715
<212> DNA
<213> Cucumis melo
<220> ← insert this
<221> misc_feature
<222> 1283
<223> n = A,T,C or G

last sequence in file

mandatory numeric identifier whenever

(2217, 22227, or 22237 is shown

<400> 56
atggctactc cttcttcctc ctccccctgaa cttcctctca aaccaattcc cgggtggctat 60
ggcttccccct tctctcggtc catcaaagac cgttacgatt acttctatatt ccaaggtaga 120
gacgaattct tccgttcccc gattaccaaa tacaactcca ccgtcttccg cgccaacatg 180
ccaccggggcc ccttcatttc ctccgattcc agagtcggtg tcttctctga tgccctcagt 240
tttctatccc tcttcgacac agccaaagtc gagaaacgca acattctcga cggaaacttac 300
atgccctcct tgtccttcac cggcaacatt cgcacctgtg cttatttgga cccatcggaa 360
acagagcact ctgttctcaa acgcctcttc ctctccttcc tgccttcccg ccatgacagg 420
ttcatccctc tgtttcgaag ctcttctgtc gagatgtttg ttaagcttga agataaactt 480
tccgagaaaa agaagatcgc tgatttcaac tcatcagcgc attccatgtc gtttgattat 540
gttttccgtt tactctccga tggaaacctt gattcgaaat tagctgctga gggacctgga 600
atgttcgctc tgttgcttgt gtttcaactc gccccattgg cttccattgg ccttcccaaa 660
atcttctctg tttttgaaga tctcgtcatt cacaccattc cctcgccttt cttcccagtc 720
aagagtgggt acaggaagct ttatgaagcg ttttactcct cttctggctc atttctagac 780
gaagcagaga aacaggggat agacagggag aaagcatgtc acaatttagt gtttctcgct 840
ggattcaacg catacggggg aatgaaagtc ctttttccca ctttactgaa atgggtcggc 900
accgccggcg aggatctcca ccgaaaactc gccgaggaag tcaggacaac cgtgaaggaa 960
gaagggggac tgactttctc cgccttgagg aaaatgagtc tgctgaagtc cgtcgtgtac 1020
gaagcactca ggatcgaacc gccggtgccg ttccagtacg ggaaagcgaa ggaggatata 1080
gtgattcaga gccacgattc ttctttcaag atcaaaaaag gggagacgat ttttggttat 1140
cagccgtttg ctactaaaga tccgaagatt ttttaaggatt cggagaagtt cgtgggcgat 1200
aggttcgtgg gagaagaagg ggagaagctt ttgaagtatg tttactggtc aaatgagcgg 1260
gagacagtgg agccgacgcg gangaacaag cagtgtccgg ggaagaatct ggtggtgctg 1320
ataggttaga ttatgggtgt ggaattcttc cttcgttatg atacgttcac cgtggaggtc 1380
gcggatttgc cgtcgggtcc ggcagtgaag ttcaagtcct taaccagagc aaccgatatg 1440
ttaaagctaa tgactaatta gttttatcat ttacagatag tgaattgggt gatgcacgga 1500
agctgtggcg gactgcccac acatgattga gtacttgggg ttattaaagt aatttcgttg 1560
tgatccacgt ggtcttattt taatttgaga tctcattgtg tgttgtaacc caccggtcat 1620
cttattttat agtttggttg ttttctcaat tatgctccaa attttaaaat aaataaatac 1680
catcttcttc ttttactaaa aaaaaaaaaa aaaaaa 1715

same
error
appears
in seq. 15

FYE

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/884,260

DATE: 07/06/2001
TIME: 11:38:52

Input Set : A:\W054316.txt
Output Set: N:\CRF3\07062001\I884260.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:334 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1326 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:56
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (57) Counted (56)